Amendments to the Claims under 37 C.F.R. § 1.121

Claims 1-7 (cancelled).

Claim 8 (currently amended): A method for detecting human papilloma virus (HPV) DNA in a cell sample which indicates the patient providing the cell sample is at risk for cancer, comprising:

(a) adding a reagent comprising a plurality of genomic HPV DNA probe sets to the cell sample under suitable hybridization conditions, wherein:

(i) a first genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 16, and which constitute approximately 8.3% of the total HPV DNA in the reagent,

(ii) a second genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 18, and which constitute approximately 20.8% of the total HPV DNA in the reagent,

(iii) a third genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 31, and which constitute approximately 8.3% of the total HPV DNA in the reagent,

(iv) a fourth genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 33, and which constitute approximately 20.8% of the total HPV DNA in the reagent,

(v) a fifth genomic HPV DNA probe set comprises a plurality of labeled nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 35, and which constitute approximately 20.8% of the total HPV DNA in the reagent, and

(vi) a sixth genomic HPV DNA probe set comprises a plurality of labeled

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nucleic acid fragments prepared by labeling essentially the full-length genomic sequence of HPV type 51, and which constitute approximately 20.8% of the total HPV DNA in the reagent;

wherein the labeled nucleic acid fragments of the genomic HPV DNA probe sets detectably hybridize to the genomic sequence of HPV types 39, 45, 52, 56, 58, 59, 68 and 70 in addition to detectably hybridizing to the genomic sequence of HPV types 16, 18, 31, 33, 35, and 51; and

wherein the labeled nucleic acid fragments of the genomic HPV DNA probe sets do not detectably hybridize to the genomic sequence of HPV types 42, 43, or 44; and

(b) determining whether the labeled nucleic acid fragments of the genomic HPV DNA probe sets detectably hybridize to HPV DNA in the cell sample.

Claim 9 (cancelled).

Claim 10 (previously presented): The method of claim 8, wherein hybridization conditions comprise washing the cell sample at 45°C in a buffer comprising 2X SSC and 2% BSA.

Claim 11 (previously presented): The method of claim 8, further comprising pretreating the cell sample with a protease.

Claim 12 (previously presented): The method of claim 8, further comprising destaining and/or deparaffining the cell sample.

Claims 13-15 (cancelled).

Claim 16 (previously presented): The method of claim 8, wherein the cell sample contains abnormal cervical cells.

Claims 17-22 (cancelled).

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Claim 23 (previously presented): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by nick translation.

Claim 24 (previously presented): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by polymerase chain reaction (PCR).

Claim 25 (previously presented): The method of claim 8, wherein the plurality of labeled nucleic acid fragments of the genomic HPV DNA probe sets are labeled by random priming.

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